

CLAIMS

1. Array for analysing a nucleic acid sequence or mixture of nucleic acid sequences, comprising:

- 5 a) a carrier; and
- b) at least two different nucleic acid sequences bound to said carrier, in which each of the nucleic acid sequences bound to the carrier comprises at least a nucleic acid sequence that corresponds to the sequence of a restriction fragment obtainable by restricting a genomic DNA and/or at least one cDNA with at least one frequent cutter restriction enzyme and at least one
- 10 rare cutter restriction enzyme.

2. Array according to claim 1, which comprises at least 10, preferably at least 100, more preferably at least 1000 different nucleic acid sequences bound to the carrier.

3. Array according to claim 1 or 2, in which each of the different nucleic acid sequences is bound to the carrier in such a way that it is attached to, and corresponds with, a distinct part of the carrier, so as to form an independently detectable area of the array.

4. Array according to any of the preceding claims, in which the density of the different nucleic acid sequences bound to the carrier is in the range of 1-100,000 different sequences/cm², preferably 5-10,000 different sequences/cm², more preferably between 10-1000 different sequences/cm².

5. Array according to any of the preceding claims, in which restriction fragment sequences present in the nucleic acid sequences bound to the carrier have a size of 10 to 1200 nucleotides, and may include partial nucleotide sequences obtained by restricting the restriction fragments generated from the starting genomic DNA and/or cDNA with one or more further restriction enzymes, and/or *de novo* synthesized oligonucleotides based thereon and/or derived thereof.

5 / 6. Array according to any of the preceding claims, in which the restriction fragments have been derived from genomic DNA, and in which at least 50%, preferably at least 70%, more preferably at least 90%, of the nucleic acid sequences bound to the carrier comprise the sequence of a restriction fragment that corresponds to an AFLP-marker.

10 7. Array according to claim 6, comprising a plurality of AFLP-markers taken from a single individual or from a group of related individuals.

15 8. Array according to claim 6 or 7, comprising several sets of AFLP-markers, in which each set comprises one or more markers taken from a single individual, wherein said sets of one or more markers have been taken from individuals belonging to a group of related individuals.

20 9. Array according to any of claims 6-8, in which the AFLP-markers have been taken from individuals belonging to the same species of plant, animal or micro-organism.

25 10. Array according to any of claims 7-9, in which the AFLP-markers have been taken from, or are representative for, different subspecies, varieties, cultivars or races of the same species.

30 11. Array according to claim 9 or 10, in which the AFLP-markers have been taken from plants including but not limited to wheat, barley, maize, tomato, pepper, lettuce or rice.

12. Array according to any of claims 6-9, in which the AFLP-markers have been taken from the human genome.

13. Array according to any of claims 1-12, and in particular according to claim

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12, in which the AFLP-markers are representative for the presence, the absence or the state of a genetically determined or influenced disease.

14. Array according to any of claims 1-5, in which the restriction fragments have been generated from one or more cDNAs.

15. Method for providing an array of nucleic acid sequences bound to a carrier, in particular an array according to any of the preceding claims, comprising the steps of:

- a) identifying an AFLP-marker;
- b) providing a nucleic acid sequence that comprises a restriction fragment sequence corresponding to said AFLP-marker;
- c) attaching the nucleic acid sequence to the carrier; and
- d) repeating steps a) to c) for different AFLP markers to build up an array.

16. Method according to claim 15, comprising the steps of:

- a) identifying a polymorphic band in an AFLP-fingerprint;
- b) isolating a nucleic acid sequence from said polymorphic band;
- c) optionally further amplifying, purifying and/or modifying the nucleic acid sequence; and
- d) attaching the nucleic acid sequence to the carrier.
- e) repeating steps a) to d) for different polymorphic bands to build up an array.

17. Method for providing an array of nucleic acid sequences bound to a carrier, in particular an array according to any of the preceding claims, comprising the steps of:

- a) providing a nucleic acid sequence that comprises at least one restriction fragment that has been derived from at least one cDNA.
- b) attaching the nucleic acid sequence to the carrier; and
- c) repeating steps a) and b) for different cDNA-derived restriction fragments to build up an array.

18. Method according to claim 17, comprising the steps of:

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- a) analysing at least one cDNA using AFLP-methodology to provide a cDNA-AFLP fingerprint, said fingerprint comprising at least one, and usually a plurality, of bands;
- b) isolating from at least one of said bands at least one nucleic acid sequence;
- c) optionally further amplifying, purifying and/or modifying the nucleic acid sequence;
- d) attaching the nucleic acid sequence to the carrier; and
- 10 e) repeating steps a) to d) for different bands and/or for different cDNAs to build up an array.

19. Array, obtainable by the method of any of claims 15-18.

20. Method for analysing a nucleic acid sequence or a mixture of nucleic acids sequences, comprising contacting said nucleic acid or mixture under hybridizing conditions with an array according to any of claims 1-14 or 19 or obtained according to the method of any of claims 15-18.

21. Method according to claim 20, in which the nucleic acid sequence or mixture is suspected to comprise at least one sequence that corresponds to a restriction fragment sequence present in the nucleic acid sequences present in the array, more specifically to an AFLP-marker present in the array.

22. Method according to claim 20 or 21, in which the nucleic acid sequence or mixture comprises DNA, in particular genomic DNA or a mixture of restriction fragments derived from genomic DNA.

23. Method according to any of claims 20-22, in which the nucleic acid sequence or mixture comprises a mixture of restriction fragments obtained by restricting a genomic DNA with the same frequent cutter restriction enzyme and rare cutter

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30. Non-processed or processed results or data obtainable by analysing a nucleic acid or mixture of nucleic acids with an array according to any of claims 1-14 or 19, or by a method according to any of claims 20-28, for instance in the form of an image, of a score, of digital or analog data, optionally stored on a suitable data carrier, including paper, photographic film, computer disc or files, or as a database.

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